

Artificial Life

Study of the Evolutionary/Pragmatics of BioSemiotics

- http://www.c3.lanl.gov/rocha/alife.html
- Life as it could be
- Abstract Simulations

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The Origin of Codes

Reproduction is Possible Without Codes

Why Are codes important for evolution?

Dynamics

Rate-Dependent Catalytic



Memory Rate-Independent Inheritable

- Both peptide [Ghadiri et al] and nucleic acid chains are capable of template replication.
 - Only a small fraction of peptide sequences can though – occasional templates. RNA is an obligatory template

Self-Inspection
Subsumes Template
Replication, which is
increasingly harder for
long chains

Self-Organizing Agents



Self-Organizing Agent



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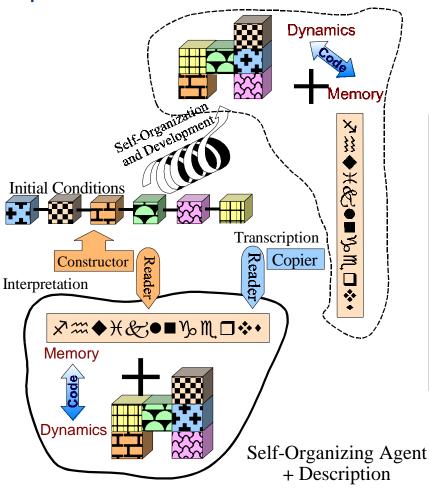
Initial Conditions

Direct Component



Coded Reproduction

Open-ended Evolution



Self-Organizing
Agent +
Description

- Can consistently produce any configuration from a stable, inheritable description
 - Not Just those whose initial conditions are recoverable
- Variation on descriptions
 - Not on phenotypes
- Can reproduce complicated, developed phenotypes
- Open-ended evolution

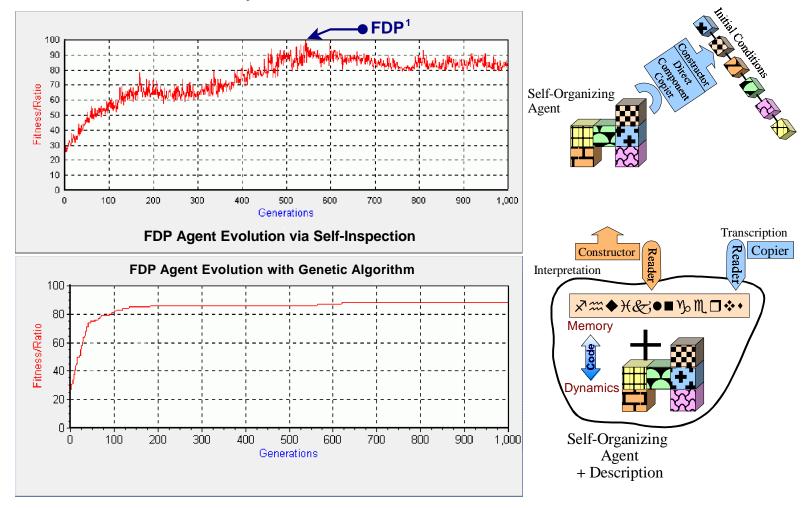
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Coded vs. Noncoded Agents

Simulations of Evolutionary Potential



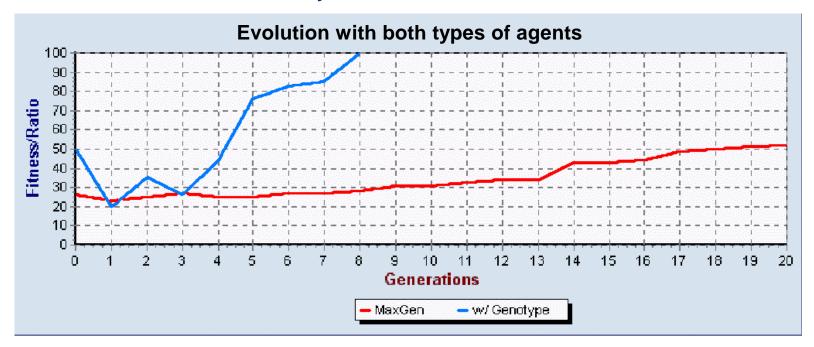
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Coded Vs. Noncoded Agents

Simulations of Evolutionary Potential



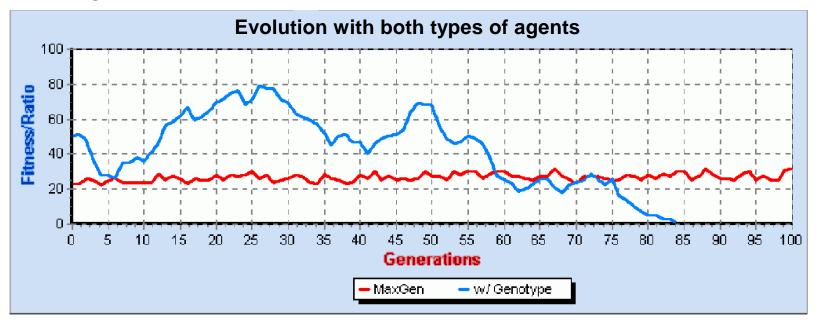
Under most conditions and types of evolutionary algorithms, coded agents overtake the population in a small number of generations. /pattee/rocha.html

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Coded vs. Noncoded Agents

With high values of variation



With too much genetic variation, the stability of descriptions is lost, resulting in occasional taking over of the population by noncoded agents.

/pattee/rocha.html

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The Origin of Codes

How would an RNA code work?

Dynamics

RNA Molecules Catalytic, functional ribozymes



Memory
RNA Molecules
Inheritable "inert

Inheritable, "inert", information carriers

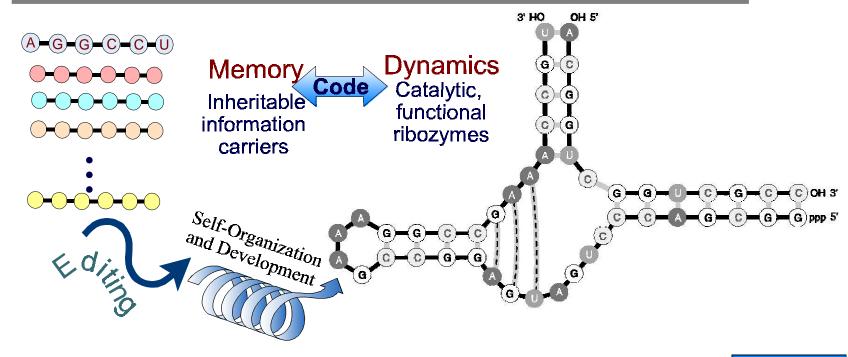
- How can a dual-function RNA molecule induce an evolutionary process?
 - ► They need to be stable (non-reactive) to carry information, while at the same time they need to be reactive to perfom some (auto) catalytic function.
- Pure catalytic world (no code)
 - Requires some reader/constructor such as the self-organizing agents of previous simulations (self-inspection)
 - Protein world would offer richer dynamics
- Template Reproduction (no code)
 - Enzyme-free template-induced synthesis of long RNA molecules from monomers has not been achieved.
 Dissociation problem.
 - ► The more complex a ribozyme is, the more difficult it is to reproduce it as a template. A reader/constructor would be needed (self-inspection)

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A Primordial RNA Editing Code?

- Inheritable RNA fragments with assembly (development) of complex catalytic ribozymes
 - ► Arts and Benne [1996] suggested RNA editing as a mechanism to integrate non-reactive, inheritable small RNA molecules into reactive ribozymes.
 - Small fragments can be ligated [von Kiedrowski, 1986]
 - ► Ribozymes show ligase [Ekland et al, 1995] and cleavage activity [Cech, 1983].



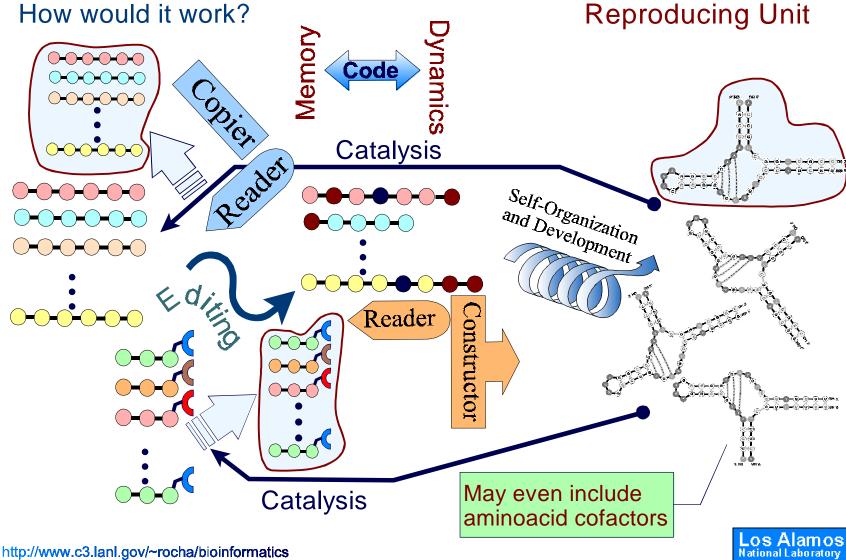
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The RNA Editing Code

The Self-Reproducing Unit



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The RNA Editing Code

How to Study it Computationally

- How easy is it to obtain a given functional RNA structure?
 - Neutral Networks of RNA Secondary Structure.
 Schuster, Stadler, Reidys, Cupal, Kopp.
 - There are typically a small set of very large Neutral networks (common structures), and a large set of very small ones.
 - The fraction of sequences folding into common structures increases with length (100% in the limit).
 - What does editing do to neutral networks?
 - Are memory/functional sequences common?
- Need of collaborative effort in biocomputing

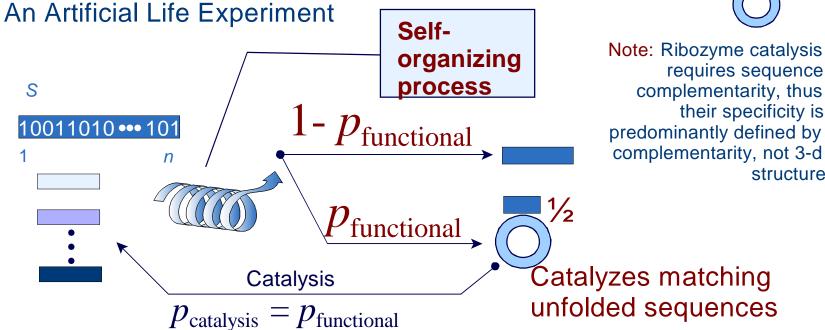
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The Sequence Editing Code



structure



Autocatalysis is possible

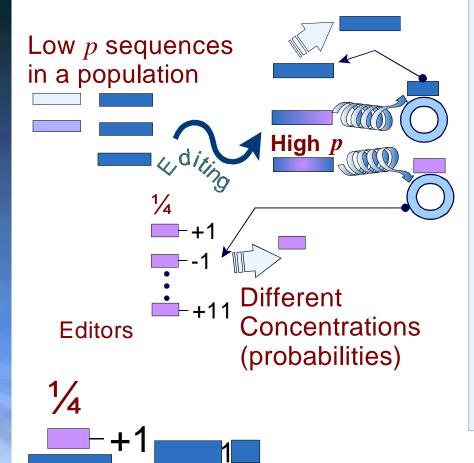
But the higher the probability and intensity of obtaining a catalyst, the lower the probability of finding an unfolded target to catalyze

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The Sequence Editing Code

Experiments



- If a family of editors is found which converts sequences from low to high p, for certain values of editors concentration, self-reproduction is viable.
 - With high concentrations, all low p sequences may be converted
- Simulations
 - Found longer complex catalytic networks highly dependent on life-span of sequences

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